

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Le, Junming
 Vilcek, Jan
 Daddona, Peter E.
 Ghrayeb, John
 Knight, David M.
 Siegel, Scott A.
- (ii) TITLE OF INVENTION: MONOCLONAL AND CHIMERIC ANTIBODIES
 SPECIFIC FOR HUMAN TUMOR NECROSIS FACTOR
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Browdy and Neimark
 (B) STREET: 419 Seventh Street, N.W.
 (C) CITY: Washington
 (D) STATE: D.C.
 (E) COUNTRY: USA
 (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0,
 Version #1.25
- (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: 08/013,413
 (B) FILING DATE: 02-FEB-1993
 (C) CLASSIFICATION: 436
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/943,852
 (B) FILING DATE: 11-SEP-1992
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/853,606
 (B) FILING DATE: 18-MAR-1992
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/670,827
 (B) FILING DATE: 18-MAR-1991
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 202-628-5197
 (B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ser | Ser | Ser | Arg | Thr | Pro | Ser | Asp | Lys | Pro | Val | Ala | His | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
20 25 30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAC	ATC	TTG	CTG	ACT	CAG	TCT	CCA	GCC	ATC	CTG	TCT	GTG	AGT	CCA	GGA	48
Asp	Ile	Leu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Val	Ser	Pro	Gly	
1				5					10					15		
GAA	AGA	GTC	AGT	TTC	TCC	TGC	AGG	GCC	AGT	CAG	TTC	GTT	GGC	TCA	AGC	96
Glu	Arg	Val	Ser	Phe	Ser	Cys	Arg	Ala	Ser	Gln	Phe	Val	Gly	Ser	Ser	
			20					25					30			
ATC	CAC	TGG	TAT	CAG	CAA	AGA	ACA	AAT	GGT	TCT	CCA	AGG	CTT	CTC	ATA	144
Ile	His	Trp	Tyr	Gln	Gln	Arg	Thr	Asn	Gly	Ser	Pro	Arg	Leu	Leu	Ile	
			35				40					45				
AAG	TAT	GCT	TCT	GAG	TCT	ATG	TCT	GGG	ATC	CCT	TCC	AGG	TTT	AGT	GGC	192
Lys	Tyr	Ala	Ser	Glu	Ser	Met	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						
AGT	GGA	TCA	GGG	ACA	GAT	TTT	ACT	CTT	AGC	ATC	AAC	ACT	GTG	GAG	TCT	240
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ser	Ile	Asn	Thr	Val	Glu	Ser	
	65				70					75				80		
GAA	GAT	ATT	GCA	GAT	TAT	TAC	TGT	CAA	CAA	AGT	CAT	AGC	TGG	CCA	TTC	288

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95

ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
100 105

321

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
100 105

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA 48
Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC 96
Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
20 25 30
TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT 144

Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 35 40 45
 GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG 192
 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 50 55 60
 TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT 240
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
 65 70 75 80
 GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT 288
 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
 85 90 95
 TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA 336
 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
 100 105 110
 GGC ACC ACT CTC ACA GTC TCC 357
 Gly Thr Thr Leu Thr Val Ser
 115

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
 20 25 30
 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
 65 70 75 80
 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
 85 90 95
 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Thr Leu Thr Val Ser
 115